



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/829,631

Source: OIPE

Date Processed by STIC: 4-23-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPF

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/829,631

DATE: 04/23/2001

TIME: 13:40:58

Input Set : A:\NIH047.1CP1C1.txt

Output Set: N:\CRF3\04232001\I829631.raw

4 <110> APPLICANT: Sibley, David R.
 5 Monsma, Frederick J.
 6 Hamblin, Mark
 9 <120> TITLE OF INVENTION: The ST-B17 Serotonin Receptor
 12 <130> FILE REFERENCE: NIH047.1CP1C1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/829,631
 C--> 15 <141> CURRENT FILING DATE: 2001-04-10
 17 <150> PRIOR APPLICATION NUMBER: US 08/428,242
 18 <151> PRIOR FILING DATE: 1995-09-18
 20 <160> NUMBER OF SEQ ID NOS: 13
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 33
 26 <212> TYPE: DNA
 27 <213> ORGANISM: (primer)
 29 <400> SEQUENCE: 1
 30 gtcgaccctk tksgecmtea kcayrgctcg cta 33
 32 <210> SEQ ID NO: 2
 33 <211> LENGTH: 35
 34 <212> TYPE: DNA
 35 <213> ORGANISM: (primer)
 37 <400> SEQUENCE: 2
 38 aagcttatga araagggcag scarcagagg kyrma 35
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 33
 42 <212> TYPE: DNA
 43 <213> ORGANISM: (primer)
 45 <400> SEQUENCE: 3
 46 aagcatagca ggaaggcctt gaaggccagc ctg 33
 48 <210> SEQ ID NO: 4
 49 <211> LENGTH: 33
 50 <212> TYPE: DNA
 51 <213> ORGANISM: (primer)
 53 <400> SEQUENCE: 4
 54 ggcgagaaat acgcccctgaa gttctcccg gac 33
 56 <210> SEQ ID NO: 5
 57 <211> LENGTH: 30
 58 <212> TYPE: DNA
 59 <213> ORGANISM: primer
 61 <400> SEQUENCE: 5
 62 ttgccaatac tactctaagg tgcagcttcc 30
 64 <210> SEQ ID NO: 6
 65 <211> LENGTH: 30
 66 <212> TYPE: DNA
 67 <213> ORGANISM: (primer)
 69 <400> SEQUENCE: 6
 70 cacacgactt aactccatag agtcgatcgg

Does Not Comply
 Corrected Diskette Needed

pp 1, 5

Valid responses for <213> are:

- 1 - Genus species of organism 33
- 2 - Artificial sequence
- 3 - Unknown 33

Unknown and artificial sequences must include <220>, <223> features to explain the source of the genetic material in the sequence.

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Input Set : A:\NIH047.1CP1C1.txt

Output Set: N:\CRF3\04232001\I829631.raw

```

72 <210> SEQ ID NO: 7
73 <211> LENGTH: 1914
74 <212> TYPE: DNA
75 <213> ORGANISM: Rat
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (439)...(1749)
81 <400> SEQUENCE: 7
82 ccaaccccc cgcgcgacac gtggtgatct aacgtactca cagccccacc cttctcgaag 60
83 agactgcccc ggccggaagg cgggagttcg gctcctgctc ccacatcccc agctgtgccc 120
84 ctageccagga accccacccc catcttatgg cctccccggg ggcctatctc catcccaggg 180
85 ctctatccca gccccaagct aactttcatt gactcgtcac atcagtaccc ctccccaaac 240
86 ttcttaccgg agtactccag gtggccctgc gtaggaggca cccctacaac tctccccgat 300
87 ctcttgaat cgtctctga tgacctaaaga accccgtttt gccataacta ctctaagggtg 360
88 cagcttcctt tctctcctt tgccttcacc ctgtacctgc agtcaccata tcccgctctg 420
89 gtcctcaacc cagtcccc'atg gtt cca gag cca ggc cct gtc aac agt agc 471
90 Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser
91 1 5 10
93 acc cca gcc tgg ggt ccc ggg cca ccg cct gct ccg ggg ggc agc ggc 519
94 Thr Pro Ala Trp Gly Pro Gly Pro Pro Ala Pro Gly Gly Ser Gly
95 15 20 25
97 tgg atg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc 567
98 Trp Val Ala Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala
99 30 35 40
101 aat tgc ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
102 Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
103 45 50 55
105 acg tct aac ttc ttt ctg gtg tgc ctc ttc acg tgc gac ttg atg gtg 663
106 Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val
107 60 65 70 75
109 ggg ttg gtg gtg atg ccc cca gcc atg ctg aac gcg ctg tat ggg cgc 711
110 Gly Leu Val Val Met Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg
111 80 85 90
113 tgg gtg tta gct cga ggc ctc tgt ctg ctt tgg act gcc ttc gac gtg 759
114 Trp Val Leu Ala Arg Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val
115 95 100 105
117 atg tgc tgc agc gcc tcc atc ctc aac ctc tgc ctc atc agc ctg gac 807
118 Met Cys Cys Ser Ala Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp
119 110 115 120
121 cgc tac ctg ctc atc ctc tgc ccg ctg cgc tac aag ctg cgc atg aca 855
122 Arg Tyr Leu Leu Ile Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr
123 125 130 135
125 gcc ccg cga gcc ctg gcg ctc atc ctg ggt gcc tgg agc ctc gcg gcg 903
126 Ala Pro Arg Ala Leu Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala
127 140 145 150 155
129 ctt gcc tcc ttc cta ccc ctc ttg ctg ggc tgg cac gaa ctg ggc aaa 951
130 Leu Ala Ser Phe Leu Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys
131 160 165 170
133 gct cga aca cct gcc cct ggc cag tgc cgc cta ttg gcc agc ctg cct 999

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```

134 Ala Arg Thr Pro Ala Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro
135      175      180      185
137 ttt gtc ctc gtg gcg tcc ggc gtc acc ttt ttc ctg cct tgc ggt gcc 1047
138 Phe Val Leu Val Ala Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala
139      190      195      200
141 atc tgc ttc acc tac tgc agg atc ctt ctg gct gcc cgc aag cag gcg 1095
142 Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala
143      205      210      215
145 gtg caa gtg gcc tgc ctc acc acg ggc acg gct ggc cag gcc ttg gaa 1143
146 Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu
147 220      225      230      235
149 acc ttg cag gtg ccc agc aca cca cgc cca ggg atg gag tcc gct gac 1191
150 Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp
151      240      245      250
153 agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc 1239
154 Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser
155      255      260      265
157 ctg acc ctg gcc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc 1287
158 Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro
159      270      275      280
161 ttc ttt gtg gcc aac ata gct cag gcc gtg tgt gac tgc atc tcc cca 1335
162 Phe Phe Val Ala Asn Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro
163      285      290      295
165 ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt aat agc acc atg 1383
166 Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met
167 300      305      310      315
169 aac cct atc atc tac ccg ctc ttt atg cgg gac ttc aag agg gcc ctg 1431
170 Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu
171      320      325      330
173 ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc acc ggc cag ccc 1479
174 Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro
175      335      340      345
177 tgc ctc ccc ctc cat gtg gac ctc tca cag cgg tgc cag acc agg cct 1527
178 Cys Leu Pro Leu His Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro
179      350      355      360
181 cag ctg cag cag gtg ctc gct ctg cct ctg ccg cca aac tca gat tca 1575
182 Gln Leu Gln Gln Val Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser
183      365      370      375
185 gac tcc gct tca ggg ggc acc tgc ggc ctg cag ctc aca gcc cag ctt 1623
186 Asp Ser Ala Ser Gly Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu
187 380      385      390      395
189 ctg ctg cct gga gag gcc aca cgg gac ccc ccg cca ccc acc agg gcc 1671
190 Leu Leu Pro Gly Glu Ala Thr Arg Asp Pro Pro Pro Pro Thr Arg Ala
191      400      405      410
193 acc act gtg gtc aac ttc ttt gtc aca gac tct gtg gag cct gag ata 1719
194 Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile
195      415      420      425
197 cgg ccg cat cca ctc agt tcc ccc gtg aac tgaccagggtc aagagctggc 1769
198 Arg Pro His Pro Leu Ser Ser Pro Val Asn

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Input Set : A:\NIH047.1CP1C1.txt

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```

199          430          435
201 cattggagggc cacattcccg gagctctcag cccactctcc ctgagactag gaggtggtag 1829
202 gtctctctgag agtgtgtga attgaggtat ctgagctagc ccatcttctg ctgcagctcc 1889
203 ttgactgagg ggtagtcaga cacat                                     1914
205 <210> SEQ ID NO: 8
206 <211> LENGTH: 437
207 <212> TYPE: PRT
208 <213> ORGANISM: Rat
210 <400> SEQUENCE: 8
211 Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser Thr Pro Ala Trp Gly
212 1 5 10 15
213 Pro Gly Pro Pro Pro Ala Pro Gly Gly Ser Gly Trp Val Ala Ala Ala
214 20 25 30
215 Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala Asn Ser Leu Leu Ile
216 35 40 45
217 Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn Thr Ser Asn Phe Phe
218 50 55 60
219 Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val Gly Leu Val Val Met
220 65 70 75 80
221 Pro Pro Ala Met Leu Asn Ala Leu Tyr Gly Arg Trp Val Leu Ala Arg
222 85 90 95
223 Gly Leu Cys Leu Leu Trp Thr Ala Phe Asp Val Met Cys Cys Ser Ala
224 100 105 110
225 Ser Ile Leu Asn Leu Cys Leu Ile Ser Leu Asp Arg Tyr Leu Leu Ile
226 115 120 125
227 Leu Ser Pro Leu Arg Tyr Lys Leu Arg Met Thr Ala Pro Arg Ala Leu
228 130 135 140
229 Ala Leu Ile Leu Gly Ala Trp Ser Leu Ala Ala Leu Ala Ser Phe Leu
230 145 150 155 160
231 Pro Leu Leu Leu Gly Trp His Glu Leu Gly Lys Ala Arg Thr Pro Ala
232 165 170 175
233 Pro Gly Gln Cys Arg Leu Leu Ala Ser Leu Pro Phe Val Leu Val Ala
234 180 185 190
235 Ser Gly Val Thr Phe Phe Leu Pro Ser Gly Ala Ile Cys Phe Thr Tyr
236 195 200 205
237 Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala Val Gln Val Ala Ser
238 210 215 220
239 Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu Thr Leu Gln Val Pro
240 225 230 235 240
241 Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp Ser Arg Arg Leu Ala
242 245 250 255
243 Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser Leu Thr Leu Gly Ile
244 260 265 270
245 Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro Phe Phe Val Ala Asn
246 275 280 285
247 Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro Gly Leu Phe Asp Val
248 290 295 300
249 Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met Asn Pro Ile Ile Tyr
250 305 310 315 320

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Output Set: N:\CRF3\04232001\I829631.raw

```

251 Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu Gly Arg Phe Leu His
252                               325                               330                               335
253 Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro Cys Leu Pro Leu His
254                               340                               345                               350
255 Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro Gln Leu Gln Gln Val
256                               355                               360                               365
257 Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser Asp Ser Ala Ser Gly
258                               370                               375                               380
259 Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu Leu Pro Gly Glu
260 385                               390                               395                               400
261 Ala Thr Arg Asp Pro Pro Pro Pro Thr Arg Ala Thr Thr Val Val Asn
262                               405                               410                               415
263 Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile Arg Pro His Pro Leu
264                               420                               425                               430
265 Ser Ser Pro Val Asn
266                               435
269 <210> SEQ ID NO: 9
270 <211> LENGTH: 2108
271 <212> TYPE: DNA
272 <213> ORGANISM: Rat
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION (439)...(1311)
278 <221> NAME/KEY: intron
279 <222> LOCATION (1312)...(1505)
281 <221> NAME/KEY: CDS
282 <222> LOCATION (1506)...(1943)
284 <400> SEQUENCE: 9
285 ccaacccccca cgcgcgacac gtggtgatct aacgtactca cacgcccacc cttctcgaag 60
286 agactgcccc gcccggaagg cgggagttcg gctcctgctc ccacatcccc agctgtgccc 120
287 ctaggccagga accccacccc catcttatgg catccccggg gccctattc catcccaggg 180
288 ctctcaccaca gcccacaagt aactttcatt gactcgteac atcagtacc ctcaccaaac 240
289 ttcttaccag agtactccag gtggccctgc gtaggaggca ccctacaac tctcccgat 300
290 ctcttgaaat cgtgctcga tgacctaga accccgtttt gccatacta ctctaagggtg 360
291 cagcttcctt tctctcctt tgccttcacc ctgtacctgc agtcaccata tcccgctctg 420
292 gtcctcaacc cagtcccc atg gtt cca gag cca ggc cct gtc aac agt agc 471
293                               Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser
294                               1                               5                               10
296 acc cca gcc tgg ggt ccc ggg cca ccg cct gct ccg ggg ggc agc ggc 519
297 Thr Pro Ala Trp Gly Pro Gly Pro Pro Ala Pro Gly Gly Ser Gly
298                               15                               20                               25
300 tgg gtg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc 567
301 Trp Val Ala Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala
302                               30                               35                               40
304 aat tcg ctg ctg atc gtg ctc att tgc acg cag ccc gcc gtg cgc aac 615
305 Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn
306                               45                               50                               55
308 acg tct aac ttc ttt ctg gtg tcg ctc ttc acg tcg gac ttg atg gtg 663
309 Thr Ser Asn Phe Phe Leu Val Ser Leu Phe Thr Ser Asp Leu Met Val

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/829,631

DATE: 04/23/2001

TIME: 13:40:59

Input Set : A:\NIH047.1CP1C1.txt

Output Set: N:\CRF3\04232001\I829631.raw

L 14 M:270 C: Current Application Number differs, Replaced Current Application Number
L 15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 12
L 509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L 609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 12
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#.13
L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#.13